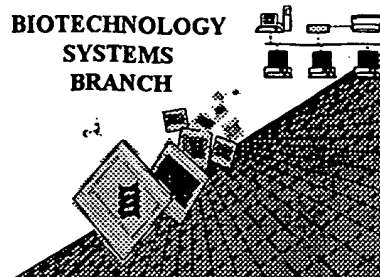


M. Walicki

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/554,414A

Source: OIP

Date Processed by STIC: 8/8/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/554,414A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos: The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 Use of <220> Sequence(s) 1-10 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIFE

RAW SEQUENCE LISTING

DATE: 08/08/2001

PATENT APPLICATION: US/09/554,414A

TIME: 14:15:37

Input Set : A:\Sequence listing.txt

Output Set: N:\CRF3\08082001\I554414A.raw

Does Not Comply
Corrected Diskette Needed

pp 1-5

W--> 13 <130> FILE REFERENCE:
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/554,414A
 C--> 15 <141> CURRENT FILING DATE: 2000-09-06
 15 <150> PRIOR APPLICATION NUMBER: CA 2,220,805
 16 <151> PRIOR FILING DATE: 1997-11-12
 18 <150> PRIOR APPLICATION NUMBER: CA 2,230,991
 19 <151> PRIOR FILING DATE: 1998-05-11
 21 <160> NUMBER OF SEQ ID NOS: 10
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1804
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Unknown see item 11 on Eva Summary Sheet

W--> 30 <220> FEATURE:
 W--> 30 <223> OTHER INFORMATION:
 30 <400> SEQUENCE: 1

```

31 ccgctctgcg ggcggggcggt gtctccggga ttccaagggc tcggttacgg aagaagcgca      60
32 gagccggctg gggagggggc tggatgcgcg cgcacccggg gggaggccgc tgctgcccgg      120
33 agcaggagga gggggagagc gcggcgggcg gcagcgggcg tggcgggcgac tccgccatag      180
34 agcagggggg ccagggcgag gcgctcgctc cgtccccggg gagcgggcgt cgacagggaag      240
35 gcgctcgggg cggcgggcgt ggccgggggg ggtggaagca ggcggcccgg ggcggcgggc      300
36 tctgtggccg tggccgtggc cgtggccggg gtcggggccg tggccggggc cggggccggg      360
37 gccgcgcccg tccccagagt ggcggcagcg gccttggcgg cgacggcgcc ggcggcgcg      420
38 gcggctgcgg cgtcggcagc ggtggcgggc tcgccccccg gcgggacccg gtccctttcc      480
39 cgtcggggag ctcggggccg gggcccaggg gaccccgggc cacggagagc gggaagagga      540
40 tggactgccc ggccctcccc cccggatgga agaaggagga agtgatccga aaatcagggc      600
41 tcagtgtctg caagagcgat gtctactact tcagtccaag tggttaagaag ttcagaagta      660
42 aacctcagct ggcaagatac ctgggaaatg ctgttgacct tagcagtttt gacttcagga      720
43 ccggcaagat gatgcctagt aaattacaga agaacaagca gagactccgg aatgaccccc      780
44 tcaatcagaa caagggtaaa ccagacctga acacaacatt gccaattaga caaactgcat      840
45 caattttcaa gcaaccagta accaaattca cgaaccaccc gagcaataag gtgaagtcag      900
46 acccccagcg gatgaatgaa caaccacgtc agcttttctg ggagaagagg ctacaaggac      960
47 ttagcgcctc agatgtaaca gaacaaatta taaaaacctt ggagctacct aaaggtcttc      1020
48 aaggagtcgg tccaggtagc aatgacgaga cccttctgtc tgctgtggcc agtgctttac      1080
49 acacaagctc tgcgcccac acaggacaag tctctgtgct cgtggaaaag aaccctgctg      1140
50 tttggcttaa cacatctcaa cccctctgca aagctttcat tgttacagat gaagacatta      1200
51 ggaaacagga agagcgagtc caacaagtac gcaagaaact ggaggaggca ctgatggccg      1260
52 acatcctgtc cggggctgcg gacacggagg aagtagacat tgacatggac agtggagatg      1320
53 aggcgtaaga atatgatcag gtaactttcg actgaccttc cccaagagca aattgctaga      1380
54 aacagaatta aaacatttcc actgggtttc gcctgtaaga aaaagtgtac ctgagcacat      1440
55 agctttttta tagcactaac caatgccttt ttagatgtat ttttgatgta tatatctatt      1500

```

RAW SEQUENCE LISTING

DATE: 08/08/2001

PATENT APPLICATION: US/09/554,414A

TIME: 14:15:37

Input Set : A:\Sequence listing.txt

Output Set: N:\CRF3\08082001\I554414A.raw

56 attccaaatg atgtttatatt tgaatcctag gacttaaaat gagtctttta taatagcaag 1560
 57 caggggccctt ccggtgcagt gcagctttga ggccagggtgc agtctactgg aaaggttagca 1620
 58 cttacgtgaa atatttgttt cccccacagt tttaataataa acagatcagg agtaccaaat 1680
 59 aagtttccca attaaagatt attatacttc actgtatata aacagatttt tatactttat 1740
 60 tgaagaaga tacctgtaca ttcttccatc atcactgtaa agacaaataa atgactatat 1800
 61 tcac 1804
 63 <210> SEQ ID NO: 2
 64 <211> LENGTH: 411
 65 <212> TYPE: PRT
 66 <213> ORGANISM: Unknown
 W--> 68 <220> FEATURE:
 W--> 68 <223> OTHER INFORMATION:
 68 <400> SEQUENCE: 2
 69 Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
 70 1 5 10 15
 71 Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
 72 20 25 30
 73 Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
 74 35 40 45
 75 Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
 76 50 55 60
 77 Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
 78 65 70 75 80
 79 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 80 85 90 95
 81 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
 82 100 105 110
 83 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
 84 115 120 125
 85 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
 86 130 135 140
 87 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
 88 145 150 155 160
 89 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
 90 165 170 175
 91 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 92 180 185 190
 93 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
 94 195 200 205
 95 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
 96 210 215 220
 97 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
 98 225 230 235 240
 99 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 100 245 250 255
 101 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 102 260 265 270
 103 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
 104 275 280 285

same env

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/554,414A

DATE: 08/08/2001
TIME: 14:15:37

Input Set : A:\Sequence listing.txt
Output Set: N:\CRF3\08082001\I554414A.raw

```

105 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
106      290                      295                      300
107 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
108      305                      310                      315                      320
109 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
110      325                      330                      335
111 Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
112      340                      345                      350
113 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
114      355                      360                      365
115 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
116      370                      375                      380
117 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
118      385                      390                      395                      400
119 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
120      405                      410

```

122 <210> SEQ ID NO: 3

123 <211> LENGTH: 1589

124 <212> TYPE: DNA

125 <213> ORGANISM: Unknown

W--> 127 <220> FEATURE:

W--> 127 <223> OTHER INFORMATION:

127 <400> SEQUENCE: 3

```

128 cacgcgcggg cgggtgggcg gagcggccccc cctagcgggg gctgtgaagc gcggggaggg      60
129 ggccgagcgg gtggcgaagc cggcgcgcgc ccggtgggg gcggaggggc gaggcccgtg      120
130 ggacagaaca gctgcggcga gtggcggcgg cggaggggagc cgaatcggcg acgagcccgg      180
131 ggggtcgcaac ttgcagaagc ggcggcgggc gcggcatcgg ccacggcggg cggaaaagcc      240
132 ggggcgcaat ggagcggaag aggtgggagt gcccggcgct cccgcagggc tgggaaaggg      300
133 aagaagtgcc caggaggtcg gggctgtcgg ccggccacag ggatgtcttt tactatagcc      360
134 ccagcgggaa gaagtccgc agcaagccac aactggcacg ttacctgggc ggatccatgg      420
135 acctcagcac cttcgacttc cgcaccggaa agatgttgat gaacaagatg aataagagtc      480
136 gccagcgtgt gcgctatgat tcttccaacc aggtcaaggg caagcctgac ctgaacaccg      540
137 cgctgcctgt acggcagact gcattccatc tcaagcaacc ggtgaccaag atcaccaacc      600
138 accccagcaa caaggtcaag agcgaccgcg agaaggcagt ggaccagccg aggcagcttt      660
139 tctgggagaa gaagctaagt ggattgagtg cctttgacat tgcagaagaa ctggtcagga      720
140 ccatggactt gcccaagggc ctgcagggag tgggccctgg ctgtacagat gagacgctgc      780
141 tgtcagccat tgcgagtgt ctacacacca gcacctgcc cattacaggc cagctctctg      840
142 cagccgtgga gaagaaccct ggtgtgtggc tgaacactgc acagccactg tgcaaagcct      900
143 tcatggtgac agatgacgac atcaggaagc aggaggagct ggtacagcag gtacggaagc      960
144 gcctggagga ggcactgatg gccgacatgc tagctcatgt ggaggagctt gcccagagacg      1020
145 gggaggcacc actggacaag gcctgtgcag aggaggaaga ggaggaggaa gaggaggagg      1080
146 aagagccgga gccagagcga gtgtagcaca ggtgccctgc ccaagtctgg gctgcagact      1140
147 gccttcagcc ttgcctggac caggtagggg ccagacctgt aggaggcagc cgtccacctc      1200
148 ctttccaaag cctcctgctt ccaggtctca gtgcagggag cccctgtgga ccttgaactc      1260
149 acttgccctt gcgctgcctg gcaggaagcc ccacactgaa agcagatgag cagtgaacca      1320
150 actgagaggc cacctggaca cagtcacctc cctgcctcct tatcatagga caaggccttg      1380
151 cttggcaccg aggagctggg agccgtgttg ggtgctggag gaagtttctg gaaacacacc      1440
152 tggctatgcc caccttatgt ccctaaggct attacaggcc agggtttggg ctgctccggc      1500
153 ccacagggct gccagcctc cccacactga gggtcagcag cccaccagga agtcactttc      1560

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/554,414A

DATE: 08/08/2001
 TIME: 14:15:37

Input Set : A:\Sequence listing.txt
 Output Set: N:\CRF3\08082001\I554414A.raw

1589

154 cttcaataaa ctgatggtag gaacttgtg
 156 <210> SEQ ID NO: 4
 157 <211> LENGTH: 291
 158 <212> TYPE: PRT
 159 <213> ORGANISM: Unknown
 W--> 161 <220> FEATURE: *same*
 W--> 161 <223> OTHER INFORMATION:
 161 <400> SEQUENCE: 4
 162 Met Glu Arg Lys Arg Trp Glu Cys Pro Ala Leu Pro Gln Gly Trp Glu
 163 1 5 10 15
 164 Arg Glu Glu Val Pro Arg Arg Ser Gly Leu Ser Ala Gly His Arg Asp
 165 20 25 30
 166 Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 167 35 40 45
 168 Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
 169 50 55 60
 170 Arg Thr Gly Lys Met Leu Met Ser Lys Met Asn Lys Ser Arg Gln Arg
 171 65 70 75 80
 172 Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
 173 85 90 95
 174 Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 175 100 105 110
 176 Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 177 115 120 125
 178 Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
 179 130 135 140
 180 Gly Leu Asn Ala Phe Asp Ile Ala Glu Glu Leu Val Lys Thr Met Asp
 181 145 150 155 160
 182 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
 183 165 170 175
 184 Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Met Pro Ile
 185 180 185 190
 186 Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
 187 195 200 205
 188 Asn Thr Thr Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Glu Asp
 189 210 215 220
 190 Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
 191 225 230 235 240
 192 Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
 193 245 250 255
 194 Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Asp Asp Asp Glu
 195 260 265 270
 196 Glu Asp Glu Glu Glu Glu Glu Glu Pro Asp Pro Asp Pro Glu Met
 197 275 280 285
 198 Glu His Val
 199 290
 201 <210> SEQ ID NO: 5
 202 <211> LENGTH: 1966
 203 <212> TYPE: DNA

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/554,414A

DATE: 08/08/2001
TIME: 14:15:37

Input Set : A:\Sequence listing.txt
Output Set: N:\CRF3\08082001\I554414A.raw

```

204 <213> ORGANISM: Unknown
W--> 206 <220> FEATURE:
W--> 206 <223> OTHER INFORMATION:
206 <400> SEQUENCE: 5
207 gggggcggtg ccccgagaag gcggagacaa gatggccgcc catagcgctt ggaggaccta      60
208 agaggcggtg gccggggcca cgccccgggc aggaggggcg ctctgtgcgc gcccgctcta      120
209 tgatgcttgc gcgcgtcccc cgcgcgcgcg gctgcggggcg gggcggttct ccgggattcc      180
210 aagggtctcg ttacggaaga agcgcagcgc cggctggggga gggggctgga tgcgcgcgca      240
211 cccgggggga ggccgctgct gcccggaagca ggaggagggg gagagtgcgg cgggcggcag      300
212 cggcgtggc ggcgactccg ccatagagca gggggggccag ggcagcgcgc tcgccccgtc      360
213 cccgtgagc ggcggtgcga gggaaggcgc tcggggcggc ggccgtggcc gggggcggtg      420
214 gaagcaggcg ggccggggcg gcggcgtctg tggccgtggc cggggccggg gccgtggccg      480
215 gggacgggga cggggccggg gccggggccg cggccgtccc ccgagtggcg gcagcggcct      540
216 tggcggcgac ggcggcggct gcggcggcg cggcagcggg ggcgcgggcg ccccccggcg      600
217 ggagccggtc cctttcccgt cggggagcgc gggggccggg cccaggggac cccggggcag      660
218 ggagagcggg aagaggatgg attgcccggc cctccccccc ggatggaaga aggaggaagt      720
219 gatccgaaaa tctgggctaa gtgctggcaa agcgatgtc tactacttca gtccaagtgg      780
220 taagaagttc agaagcaagc ctcagttgcc aaggtacctg ggaaatactg ttgatctcag      840
221 cagttttgac ttcagaactg gaaagatgat gcctagtaaa ttacagaaga acaaacagag      900
222 actgcgaaac gatcctctca atcaaaaataa gggtaaacca gacttgaata caacattgcc      960
223 aattagacaa acagcatcaa ttttcaaaca accggtaacc aaagtcacaa atcatcctag     1020
224 taataaagtg aaatcagacc cacaacgaat gaatgaacag ccacgtcagc ttttctggga     1080
225 gaagaggcta caaggactta gtgcatcaga tgtaacagaa caaattataa aaaccatgga     1140
226 actacccaaa ggtcttcaag gagttggtcc aggtagcaat gatgagacc ttttatctgc     1200
227 tgttgccagt gctttgcaca caagctctgc gccaatcaca gggcaagtct ccgctgctgt     1260
228 ggaaaagaac cctgctgttt ggcttaacac atctcaaccc ctctgcaaag cttttattgt     1320
229 cacagatgaa gacatcagga aacaggaaga gcgagtacag caagtacgca agaaattgga     1380
230 agaagcactg atggcagaca tctgtcgcg agctgctgat acagaagaga tggatattga     1440
231 aatggacagt ggagatgaag cctaagaata tgatcaggta actttcgacc gactttcccc     1500
232 aagrgaaaat tcctagaaat tgaacaaaaa tgtttccact ggcttttgcc tgtaagaaaa     1560
233 aaaatgtacc cgagcacata gagcttttta atagcactaa ccaatgcctt tttagatgta     1620
234 tttttgatgt atatatctat tattcaaaaa atcatgttta ttttgagtc taggacttaa     1680
235 aattagtctt ttgtaatatc aagcaggacc ctaagatgaa gctgagcttt tgatgccagg     1740
236 tgcaatctac tggaatgta gcacttacgt aaaacatttg tttccccac agttttaata     1800
237 agaacagatc aggaattcta aataaatttc ccagttaaag attattgtga cttcactgta     1860
238 tataaacata tttttatact ttattgaaag gggacacctg tacattcttc catcatcact     1920
239 gtaaagacaa ataaatgatt atattcacaa aaaaaaaaaa aaaaaa     1966
241 <210> SEQ ID NO: 6
242 <211> LENGTH: 414
243 <212> TYPE: PRT
244 <213> ORGANISM: Unknown
W--> 246 <220> FEATURE:
W--> 246 <223> OTHER INFORMATION:
246 <400> SEQUENCE: 6
247 Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
248 1 5 10 15
249 Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
250 20 25 30
251 Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly

```

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/554,414A

DATE: 08/08/2001

TIME: 14:15:38

Input Set : A:\Sequence listing.txt

Output Set: N:\CRF3\08082001\I554414A.raw

L:13 M:201 W: Mandatory field data missing, FILE REFERENCE
L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:30 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:68 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:68 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:127 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:127 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:161 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:161 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:206 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:206 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:246 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:246 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:305 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:305 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:352 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:352 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:395 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:395 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:403 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:403 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: